

SEQUENCE LISTING

RECEIVED
OCT 12 2001
TECH CENTER 1600/2900

(1) GENERAL INFORMATION:

- (i) APPLICANT: Pastan, Ira
Chang, Kai
- (ii) TITLE OF INVENTION: Mesothelin, a Differentiation Antigen
Present on Mesothelium, Mesotheliomas and Ovarian Cancers
and Methods and Kits for Targeting the Antigen
- (iii) NUMBER OF SEQUENCES: 8
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Townsend and Townsend and Crew LLP
(B) STREET: Two Embarcadero Center, Eighth Floor
(C) CITY: San Francisco
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94111-3834
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: Not yet assigned
(B) FILING DATE: Not yet assigned
(C) CLASSIFICATION:
- B 34* (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/776,271
(B) FILING DATE: 01-DEC-1998
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: WO PCT/US97/00224
(B) FILING DATE: 03-JAN-1997
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 60/010,166
(B) FILING DATE: 05-JAN-1996
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Faris, Susan K.
(B) REGISTRATION NUMBER: 41,739
(C) REFERENCE/DOCKET NUMBER: 015280-259110US
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (415) 576-0200
(B) TELEFAX: (415) 576-0300

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2138 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 100..1986

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:


AGGAATTCCG GTGGCCGGCC ACTCCCGTCT GCTGTGACGC GCGGACAGAG AGCTACCGGT 60

GGACCCACGG TGCCTCCCTC CCTGGGATCT ACACAGACC ATG GCC TTG CAA CGG 114
Met Ala Leu Gln Arg
1 5

CTC GAC CCC TGT TGG TCC TGT GGG GAC CGC CCT GGC AGC CTC CTG TTC 162
Leu Asp Pro Cys Trp Ser Cys Gly Asp Arg Pro Gly Ser Leu Leu Phe
10 15 20

CTG CTC TTC AGC CTC GGA TGG GTG CAT CCC GCG AGG ACC CTG GCT GGA 210
Leu Leu Phe Ser Leu Gly Trp Val His Pro Ala Arg Thr Leu Ala Gly
25 30 35

GAG ACA GGG ACG GAG TCT GCC CCC CTG GGG GGA GTC CTG ACA ACC CCC 258
Glu Thr Gly Thr Glu Ser Ala Pro Leu Gly Gly Val Leu Thr Thr Pro
40 45 50

 CAT AAC ATT TCC AGC CTC TCC CCT CGC CAA CTC CTT GGC TTC CCG TGT 306
His Asn Ile Ser Ser Leu Ser Pro Arg Gln Leu Leu Gly Phe Pro Cys
55 60 65

GCG GAG GTG TCC GGC CTG AGC ACG GAG CGT GTC CGG GAG CTG GCT GTG 354
Ala Glu Val Ser Gly Leu Ser Thr Glu Arg Val Arg Glu Leu Ala Val
70 75 80 85

GCC TTG GCA CAG AAG AAT GTC AAG CTC TCA ACA GAG CAG CTG CGC TGT 402
Ala Leu Ala Gln Lys Asn Val Lys Leu Ser Thr Glu Gln Leu Arg Cys
90 95 100

CTG GCT CAC CGG CTC TCT GAG CCC CCC GAG GAC CTG GAC GCC CTC CCA 450
Leu Ala His Arg Leu Ser Glu Pro Pro Glu Asp Leu Asp Ala Leu Pro
105 110 115

TTG GAC CTG CTG CTA TTC CTC AAC CCA GAT GCG TTC TCG GGG CCC CAG 498
Leu Asp Leu Leu Leu Phe Leu Asn Pro Asp Ala Phe Ser Gly Pro Gln
120 125 130

GCC TGC ACC CGT TTC TTC TCC CGC ATC ACG AAG GCC AAT GTG GAC CTG 546
Ala Cys Thr Arg Phe Phe Ser Arg Ile Thr Lys Ala Asn Val Asp Leu
135 140 145

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| CTC | CCG | AGG | GGG | GCT | CCC | GAG | CGA | CAG | CGG | CTG | CTG | CCT | GCG | GCT | CTG | 594 |
| Leu | Pro | Arg | Gly | Ala | Pro | Glu | Arg | Gln | Arg | Leu | Leu | Pro | Ala | Ala | Leu | |
| 150 | | | | | 155 | | | | | 160 | | | | | 165 | |
| GCC | TGC | TGG | GGT | GTG | CGG | GGG | TCT | CTG | CTG | AGC | GAG | GCT | GAT | GTG | CGG | 642 |
| Ala | Cys | Trp | Gly | Val | Arg | Gly | Ser | Leu | Leu | Ser | Glu | Ala | Asp | Val | Arg | |
| | | | 170 | | | | | | 175 | | | | | 180 | | |
| GCT | CTG | GGA | GGC | CTG | GCT | TGC | GAC | CTG | CCT | GGG | CGC | TTT | GTG | GCC | GAG | 690 |
| Ala | Leu | Gly | Gly | Leu | Ala | Cys | Asp | Leu | Pro | Gly | Arg | Phe | Val | Ala | Glu | |
| | | | 185 | | | | | 190 | | | | | 195 | | | |
| TCG | GCC | GAA | GTG | CTG | CTA | CCC | CGG | CTG | GTG | AGC | TGC | CCG | GGA | CCC | CTG | 738 |
| Ser | Ala | Glu | Val | Leu | Leu | Pro | Arg | Leu | Val | Ser | Cys | Pro | Gly | Pro | Leu | |
| | | 200 | | | | | 205 | | | | | 210 | | | | |
| GAC | CAG | GAC | CAG | CAG | GAG | GCA | GCC | AGG | GCG | GCT | CTG | CAG | GGC | GGG | GGA | 786 |
| Asp | Gln | Asp | Gln | Gln | Glu | Ala | Ala | Arg | Ala | Ala | Leu | Gln | Gly | Gly | Gly | |
| | 215 | | | | | 220 | | | | | 225 | | | | | |
| CCC | CCC | TAC | GGC | CCC | CCG | TCG | ACA | TGG | TCT | GTC | TCC | ACG | ATG | GAC | GCT | 834 |
| Pro | Pro | Tyr | Gly | Pro | Pro | Ser | Thr | Trp | Ser | Val | Ser | Thr | Met | Asp | Ala | |
| 230 | | | | | 235 | | | | | 240 | | | | | 245 | |
| CTG | CGG | GGC | CTG | CTG | CCC | GTG | CTG | GGC | CAG | CCC | ATC | ATC | CGC | AGC | ATC | 882 |
| Leu | Arg | Gly | Leu | Leu | Pro | Val | Leu | Gly | Gln | Pro | Ile | Ile | Arg | Ser | Ile | |
| | | | 250 | | | | | | 255 | | | | | 260 | | |
| CCG | CAG | GGC | ATC | GTG | GCC | GCG | TGG | CGG | CAA | CGC | TCC | TCT | CGG | GAC | CCA | 930 |
| Pro | Gln | Gly | Ile | Val | Ala | Ala | Trp | Arg | Gln | Arg | Ser | Ser | Arg | Asp | Pro | |
| | | | 265 | | | | | 270 | | | | | 275 | | | |
| TCC | TGG | CGG | CAG | CCT | GAA | CGG | ACC | ATC | CTC | CGG | CCG | CGG | TTC | CGG | CGG | 978 |
| Ser | Trp | Arg | Gln | Pro | Glu | Arg | Thr | Ile | Leu | Arg | Pro | Arg | Phe | Arg | Arg | |
| | | 280 | | | | | 285 | | | | | 290 | | | | |
| GAA | GTG | GAG | AAG | ACA | GCC | TGT | CCT | TCA | GGC | AAG | AAG | GCC | CGC | GAG | ATA | 1026 |
| Glu | Val | Glu | Lys | Thr | Ala | Cys | Pro | Ser | Gly | Lys | Lys | Ala | Arg | Glu | Ile | |
| | 295 | | | | | 300 | | | | | 305 | | | | | |
| GAC | GAG | AGC | CTC | ATC | TTC | TAC | AAG | AAG | TGG | GAG | CTG | GAA | GCC | TGC | GTG | 1074 |
| Asp | Glu | Ser | Leu | Ile | Phe | Tyr | Lys | Lys | Trp | Glu | Leu | Glu | Ala | Cys | Val | |
| 310 | | | | | 315 | | | | | 320 | | | | | 325 | |
| GAT | GCG | GCC | CTG | CTG | GCC | ACC | CAG | ATG | GAC | CGC | GTG | AAC | GCC | ATC | CCC | 1122 |
| Asp | Ala | Ala | Leu | Leu | Ala | Thr | Gln | Met | Asp | Arg | Val | Asn | Ala | Ile | Pro | |
| | | | | 330 | | | | | 335 | | | | | 340 | | |
| TTC | ACC | TAC | GAG | CAG | CTG | GAC | GTC | CTA | AAG | CAT | AAA | CTG | GAT | GAG | CTC | 1170 |
| Phe | Thr | Tyr | Glu | Gln | Leu | Asp | Val | Leu | Lys | His | Lys | Leu | Asp | Glu | Leu | |
| | | | 345 | | | | 350 | | | | | | 355 | | | |
| TAC | CCA | CAA | GGT | TAC | CCC | GAG | TCT | GTG | ATC | CAG | CAC | CTG | GGC | TAC | CTC | 1218 |
| Tyr | Pro | Gln | Gly | Tyr | Pro | Glu | Ser | Val | Ile | Gln | His | Leu | Gly | Tyr | Leu | |
| | | 360 | | | | | 365 | | | | | 370 | | | | |
| TTC | CTC | AAG | ATG | AGC | CCT | GAG | GAC | ATT | CGC | AAG | TGG | AAT | GTG | ACG | TCC | 1266 |
| Phe | Leu | Lys | Met | Ser | Pro | Glu | Asp | Ile | Arg | Lys | Trp | Asn | Val | Thr | Ser | |
| | 375 | | | | | 380 | | | | | 385 | | | | | |

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|---|------|
| CTG GAG ACC CTG AAG GCT TTG CTT GAA GTC GAC AAA GGG CAC GAA ATG | 1314 |
| Leu Glu Thr Leu Lys Ala Leu Leu Glu Val Asp Lys Gly His Glu Met | |
| 390 395 400 405 | |
| AGT CCT CAG GCT CCT CGG CGG CCC CTC CCA CAG GTG GCC ACC CTG ATC | 1362 |
| Ser Pro Gln Ala Pro Arg Arg Pro Leu Pro Gln Val Ala Thr Leu Ile | |
| 410 415 420 | |
| GAC CGC TTT GTG AAG GGA AGG GGC CAG CTA GAC AAA GAC ACC CTA GAC | 1410 |
| Asp Arg Phe Val Lys Gly Arg Gly Gln Leu Asp Lys Asp Thr Leu Asp | |
| 425 430 435 | |
| ACC CTG ACC GCC TTC TAC CCT GGG TAC CTG TGC TCC CTC AGC CCC GAG | 1458 |
| Thr Leu Thr Ala Phe Tyr Pro Gly Tyr Leu Cys Ser Leu Ser Pro Glu | |
| 440 445 450 | |
| GAG CTG AGC TCC GTG CCC CCC AGC AGC ATC TGG GCG GTC AGG CCC CAG | 1506 |
| Glu Leu Ser Ser Val Pro Pro Ser Ser Ile Trp Ala Val Arg Pro Gln | |
| 455 460 465 | |
| GAC CTG GAC ACG TGT GAC CCA AGG CAG CTG GAC GTC CTC TAT CCC AAG | 1554 |
| Asp Leu Asp Thr Cys Asp Pro Arg Gln Leu Asp Val Leu Tyr Pro Lys | |
| 470 475 480 485 | |
| GCC CGC CTT GCT TTC CAG AAC ATG AAC GGG TCC GAA TAC TTC GTG AAG | 1602 |
| Ala Arg Leu Ala Phe Gln Asn Met Asn Gly Ser Glu Tyr Phe Val Lys | |
| 490 495 500 | |
| ATC CAG TCC TTC CTG GGT GGG GCC CCC ACG GAG GAT TTG AAG GCG CTC | 1650 |
| Ile Gln Ser Phe Leu Gly Gly Ala Pro Thr Glu Asp Leu Lys Ala Leu | |
| 505 510 515 | |
| AGT CAG CAG AAT GTG AGC ATG GAC TTG GCC ACG TTC ATG AAG CTG CGG | 1698 |
| Ser Gln Gln Asn Val Ser Met Asp Leu Ala Thr Phe Met Lys Leu Arg | |
| 520 525 530 | |
| ACG GAT GCG GTG CTG CCG TTG ACT GTG GCT GAG GTG CAG AAA CTT CTG | 1746 |
| Thr Asp Ala Val Leu Pro Leu Thr Val Ala Glu Val Gln Lys Leu Leu | |
| 535 540 545 | |
| GGA CCC CAC GTG GAG GGC CTG AAG GCG GAG GAG CCG CAC CGC CCG GTG | 1794 |
| Gly Pro His Val Glu Gly Leu Lys Ala Glu Glu Arg His Arg Pro Val | |
| 550 555 560 565 | |
| CGG GAC TGG ATC CTA CGG CAG CGG CAG GAC GAC CTG GAC ACG CTG GGG | 1842 |
| Arg Asp Trp Ile Leu Arg Gln Arg Gln Asp Asp Leu Asp Thr Leu Gly | |
| 570 575 580 | |
| CTG GGG CTA CAG GGC GGC ATC CCC AAC GGC TAC CTG GTC CTA GAC CTC | 1890 |
| Leu Gly Leu Gln Gly Gly Ile Pro Asn Gly Tyr Leu Val Leu Asp Leu | |
| 585 590 595 | |
| AGC GTG CAA GAG ACC CTC TCG GGG ACG CCC TGC CTC CTA GGA CCT GGA | 1938 |
| Ser Val Gln Glu Thr Leu Ser Gly Thr Pro Cys Leu Leu Gly Pro Gly | |
| 600 605 610 | |
| CCT GTT CTC ACC GTC CTG GCA CTG CTC CTA GCC TCC ACC CTG GCC | 1983 |
| Pro Val Leu Thr Val Leu Ala Leu Leu Leu Ala Ser Thr Leu Ala | |
| 615 620 625 | |
| TGAGGGCCCC ACTCCCTTGC TGGCCCCAGC CCTGCTGGGG ATCCCCGCCT GGCCAGGAGC | 2043 |

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AGGCACGGGT GATCCCCGTT CCACCCCAAG AGAACTCGCG CTCAGTAAAC GGGAACATGC 2103
 CCCCTGCAGA CAAAAAAAAA AAAAAAAAAA AAAAA 2138

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 628 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Leu Gln Arg Leu Asp Pro Cys Trp Ser Cys Gly Asp Arg Pro
 1 5 10 15
 Gly Ser Leu Leu Phe Leu Leu Phe Ser Leu Gly Trp Val His Pro Ala
 20 25 30
 Arg Thr Leu Ala Gly Glu Thr Gly Thr Glu Ser Ala Pro Leu Gly Gly
 35 40 45
 Val Leu Thr Thr Pro His Asn Ile Ser Ser Leu Ser Pro Arg Gln Leu
 50 55 60
 Leu Gly Phe Pro Cys Ala Glu Val Ser Gly Leu Ser Thr Glu Arg Val
 65 70 75 80
 Arg Glu Leu Ala Val Ala Leu Ala Gln Lys Asn Val Lys Leu Ser Thr
 85 90 95
 Glu Gln Leu Arg Cys Leu Ala His Arg Leu Ser Glu Pro Pro Glu Asp
 100 105 110
 Leu Asp Ala Leu Pro Leu Asp Leu Leu Leu Phe Leu Asn Pro Asp Ala
 115 120 125
 Phe Ser Gly Pro Gln Ala Cys Thr Arg Phe Phe Ser Arg Ile Thr Lys
 130 135 140
 Ala Asn Val Asp Leu Leu Pro Arg Gly Ala Pro Glu Arg Gln Arg Leu
 145 150 155 160
 Leu Pro Ala Ala Leu Ala Cys Trp Gly Val Arg Gly Ser Leu Leu Ser
 165 170 175
 Glu Ala Asp Val Arg Ala Leu Gly Gly Leu Ala Cys Asp Leu Pro Gly
 180 185 190
 Arg Phe Val Ala Glu Ser Ala Glu Val Leu Leu Pro Arg Leu Val Ser
 195 200 205
 Cys Pro Gly Pro Leu Asp Gln Asp Gln Gln Glu Ala Ala Arg Ala Ala
 210 215 220
 Leu Gln Gly Gly Gly Pro Pro Tyr Gly Pro Pro Ser Thr Trp Ser Val
 225 230 235 240

Ser Thr Met Asp Ala Leu Arg Gly Leu Leu Pro Val Leu Gly Gln Pro
 245 250 255
 Ile Ile Arg Ser Ile Pro Gln Gly Ile Val Ala Ala Trp Arg Gln Arg
 260 265 270
 Ser Ser Arg Asp Pro Ser Trp Arg Gln Pro Glu Arg Thr Ile Leu Arg
 275 280 285
 Pro Arg Phe Arg Arg Glu Val Glu Lys Thr Ala Cys Pro Ser Gly Lys
 290 295 300
 Lys Ala Arg Glu Ile Asp Glu Ser Leu Ile Phe Tyr Lys Lys Trp Glu
 305 310 315 320
 Leu Glu Ala Cys Val Asp Ala Ala Leu Leu Ala Thr Gln Met Asp Arg
 325 330 335
 Val Asn Ala Ile Pro Phe Thr Tyr Glu Gln Leu Asp Val Leu Lys His
 340 345 350
 Lys Leu Asp Glu Leu Tyr Pro Gln Gly Tyr Pro Glu Ser Val Ile Gln
 355 360 365
 His Leu Gly Tyr Leu Phe Leu Lys Met Ser Pro Glu Asp Ile Arg Lys
 370 375 380
 Trp Asn Val Thr Ser Leu Glu Thr Leu Lys Ala Leu Leu Glu Val Asp
 385 390 395 400
 Lys Gly His Glu Met Ser Pro Gln Ala Pro Arg Arg Pro Leu Pro Gln
 405 410 415
 Val Ala Thr Leu Ile Asp Arg Phe Val Lys Gly Arg Gly Gln Leu Asp
 420 425 430
 Lys Asp Thr Leu Asp Thr Leu Thr Ala Phe Tyr Pro Gly Tyr Leu Cys
 435 440 445
 Ser Leu Ser Pro Glu Glu Leu Ser Ser Val Pro Pro Ser Ser Ile Trp
 450 455 460
 Ala Val Arg Pro Gln Asp Leu Asp Thr Cys Asp Pro Arg Gln Leu Asp
 465 470 475 480
 Val Leu Tyr Pro Lys Ala Arg Leu Ala Phe Gln Asn Met Asn Gly Ser
 485 490 495
 Glu Tyr Phe Val Lys Ile Gln Ser Phe Leu Gly Gly Ala Pro Thr Glu
 500 505 510
 Asp Leu Lys Ala Leu Ser Gln Gln Asn Val Ser Met Asp Leu Ala Thr
 515 520 525
 Phe Met Lys Leu Arg Thr Asp Ala Val Leu Pro Leu Thr Val Ala Glu
 530 535 540
 Val Gln Lys Leu Leu Gly Pro His Val Glu Gly Leu Lys Ala Glu Glu
 545 550 555 560

B7
 nf

[illegible]

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 5 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Gly Gly Gly Gly Ser
1 5

B² (2)

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 5 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Arg Glu Asp Leu Lys
1 5

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Arg Glu Asp Leu
1

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Arg Asp Glu Leu
1

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

BZ ✓ (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Lys Asp Glu Leu
1

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Arg Pro Arg Phe Arg Arg
1 5
